

Trafficking Computes



Ivo F. Sbalzarini

Center of Systems Biology Dresden, Max Planck Institute of Molecular Cell Biology and Genetics

The functioning of cells is intimately linked to uptake, processing, and release of a multitude of signals. Cellular trafficking is key to this information processing, involving localized biochemistry in multiple dynamic compartments with still-elusive molecular and biophysical details. Concerted trafficking of chemical signals between compartments allows the cell to “compute,” i.e., to exchange information and take decisions. But this type of computation is fundamentally different from that in human-made computers.

Cellular trafficking has thus inspired the theoretical concept of membrane computing, also named “**P-Systems**” after **G. Păun**. A membrane-computing system, like the trafficking system in cells, processes a multitude of signals in parallel and in a distributed manner. It consists of many membrane-bound compartments, within which signals are processed, and which are able to move, fuse, and split, hence communicating. This concurrent, stochastic processing is conceptually different from the sequential, deterministic working of electronic computers. Systems approaches such as **P-Systems** may thus help address questions so far unanswered: What can a cell compute? Does the cellular trafficking system have a defined state, or does it probe multiple states at once? Can we unravel the rules of its working by watching it with computational imaging methods? The pioneering work by the Nobel Laureates hence continues to inspire questions and progress across discipline boundaries.